Amendments to the Claims:

This listing of claims replaces all prior versions and listings of claims in the application:

Listing of Claims:

1-13. (Canceled)

14. (New) A method for determining the presence or absence of a single nucleotide polymorphism (SNP) in a $P2X_7$ gene, the method comprising:

(a) providing a nucleic acid sample from a human identified as in need of treatment with a therapeutic agent that is transported by $P2X_7$, wherein the sample comprises a nucleotide at a position corresponding to position 1513 of SEQ ID NO:2, and

(b) testing the sample to determine the identity of the nucleotide.

15. (New) The method of claim 14, wherein the nucleic acid sample comprises a fragment of a $P2X_7$ DNA.

16. (New) The method of claim 14, wherein step (b) comprises performing a method selected from the group consisting of an ARMS™ or ALEX™ assay, COPS, Taqman™, Molecular Beacons, RFLP, restriction site based PCR and FRET.

17. (New) The method of claim 14, wherein the nucleotide is a C.

18. (New) The method of claim 14, wherein the nucleotide is not an A.

19. (New) The method of claim 14, wherein the nucleotide is in a codon that does not encode a glutamate.

20. (New) The method of claim 14, wherein the nucleotide is in a codon that encodes an alanine.

21. (New) The method of claim 14, further comprising:

(c) administering an effective amount of the therapeutic agent to the human.

22. (New) A method for determining the presence or absence of a SNP in a $P2X_7$ gene, the method comprising:

(a) providing a nucleic acid sample from a human having or at risk for developing a $P2X_7$-mediated disease, wherein the sample comprises a nucleotide at a position corresponding to position 1513 of SEQ ID NO:2; and

(b) testing the sample to determine the identity of the nucleotide.

23. (New) The method of claim 22, wherein the disease is hyperlipoproteinemia or cardiovascular disease.

24. (New) The method of claim 22, wherein step (b) comprises performing a method selected from the group consisting of an ARMS™ or ALEX™ assay, COPS, Taqman™, Molecular Beacons, RFLP, restriction site based PCR and FRET.

25. (New) A method to assess the pharmacogenetics of a drug, the method comprising

(a) providing a nucleic acid sample from a human having or at risk for developing a $P2X_7$-mediated disease, wherein the sample comprises a nucleotide at a position corresponding to position 1513 of SEQ ID NO:2;

(b) determining the identity of the nucleotide; and

(c) correlating (i) the identity of the nucleotide to (ii) the human's response following administration of the drug, thereby assessing the pharmacogenetics of the drug.

26. (New) A method of treatment comprising:

(a) identifying a patient as having or at risk for developing a $P2X_7$-mediated disease;

(b) determining the identity of the nucleotide at the position corresponding to position 1513 of SEQ ID NO:2 in a nucleic acid sample of the patient; and

(c) administering to the patient an effective amount of a therapeutic agent transportable by $P2X_7$, wherein the therapeutic agent is selected according to whether the nucleotide at the position corresponding to position 1513 of SEQ ID NO:2 is a C or is not a C.

27. (New) The method of claim 26, wherein step (b) comprises:

(i) providing a nucleic acid sample from the patient, wherein the sample comprises a nucleotide at a position corresponding to position 1513 of SEQ ID NO:2; and

(ii) determining the identity of the nucleotide by use of a method selected from the group consisting of an ARMS™ or ALEX™ assay, COPS, Taqman™, Molecular Beacons, RFLP, restriction site based PCR or FRET.

28. (New) The method of claim 26, wherein the nucleotide is a C.

29. (New) The method of claim 26, wherein the nucleotide is not an A.

30. (New) The method of claim 26, wherein the disease is hyperlipoproteinemia or cardiovascular disease.

31. (New) A method of performing a linkage study, the method comprising

(a) providing a nucleic acid sample from each of two or more humans having or at risk for having a $P2X_7$-mediated disease, wherein each of the samples comprises a nucleotide at a position corresponding to position 1513 of SEQ ID NO:2;

(b) testing each sample to determine the identity of the nucleotide in each sample; and

(c) comparing (i) the frequency with which a C occurs at the position corresponding to position 1513 of SEQ ID NO:2 in the samples, with (ii) the frequency with which C occurs at the position corresponding to position 1513 of SEQ ID NO:2 in nucleic acid samples from the population at large.

32. (New) A method for determining the presence or absence of a SNP in a $P2X_7$ gene, the method comprising:

(a) providing a nucleic acid sample from a human identified as having or at risk for developing a $P2X_7$-mediated disease, wherein the sample comprises a nucleotide at each of the following nucleotide positions:

positions 936, 1012, 1147, 1343 and 1476 as defined by the positions in SEQ ID NO:1;

positions 253, 488, 489, 760, 835, 853, 1068, 1096, 1315, 1324, 1405, 1448, 1494, 1513, 1628 and 1772 as defined by the positions in SEQ ID NO:2; and

positions 4780, 4845, 4849, 5021, 5554, 5579, 5535, 5845 and 6911 as defined by the positions in SEQ ID NO:3; and

(b) testing the sample to determine the identity of the nucleotide at position 1513 of SEQ ID NO: 2 and at one or more of the other listed nucleotide positions.

33. (New) A method for determining the presence or absence of a SNP in a $P2X_7$ gene, the method comprising

(a) providing a nucleic acid sample from a human having or at risk for developing a $P2X_7$-mediated disease, wherein the sample comprises a nucleotide at each of the following 30 positions:

positions 936, 1012, 1147, 1343 and 1476 as defined by the positions in SEQ ID NO:1;

positions 253, 488, 489, 760, 835, 853, 1068, 1096, 1315, 1324, 1405, 1448, 1494, 1513, 1628 and 1772 as defined by the positions in SEQ ID NO:2; and

positions 4780, 4845, 4849, 5021, 5554, 5579, 5535, 5845 and 6911 as defined by the positions in SEQ ID NO:3; and

(b) testing the sample to determine the identity of the nucleotide at each of the 30 positions.

34. (New) A method for determining the presence or absence of a SNP in a $P2X_7$ gene, the method comprising

(a) providing a nucleic acid sample from a human having or at risk for developing a $P2X_7$-mediated disease, wherein the sample comprises a nucleotide at each of the following 30 positions:

positions 936, 1012, 1147, 1343 and 1476 as defined by the positions in SEQ ID NO:1;

positions 253, 488, 489, 760, 835, 853, 1068, 1096, 1315, 1324, 1405, 1448, 1494, 1513, 1628 and 1772 as defined by the positions in SEQ ID NO:2; and

positions 4780, 4845, 4849, 5021, 5554, 5579, 5535, 5845 and 6911 as defined by the positions in SEQ ID NO:3; and

(b) testing the sample to determine the identity of the nucleotide at one or more of the 30 positions.